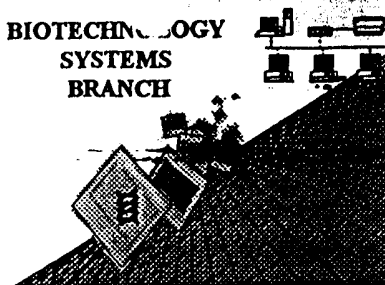


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/658,835

Source: OIPE

Date Processed by STIC: 9-22-00

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/658,835

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US 09/658,835

DATE: 09/22/2000  
 TIME: 14:59:33

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 Output Set: N:\CRF3\09222000\1658835.raw

Original Entry  
 Corrected Entry

pp. 6, 7

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1 <110> APPLICANT: Durick, Jonathan P.
2      Gilliam, Jacob T.
3      Maddox, Joyce R.
4      Rao, Pragnya Gururaj
5      Crasta, Oswald R.
6      Folkerts, Otto
11 <120> TITLE OF INVENTION: Amino Polycl Amine Oxidase
12      Polynucleotides and Related Polypeptides and Methods of Use
13 <130> FILE REFERENCE: 1134R
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17 <150> PRIOR APPLICATION NUMBER: US 60/2062,936
18 <151> PRIOR FILING DATE: 11-07-99
20 <150> PRIOR APPLICATION NUMBER: US 60/215,391
21 <151> PRIOR FILING DATE: 11-05-99
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23 <151> PRIOR FILING DATE: 11-07-99
24 <150> PRIOR APPLICATION NUMBER: US 09/452,168
25 <151> PRIOR FILING DATE: 1999-07-12
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46      ggaagacgac cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct      240
47      tgcctatgta gccacaggata gaattttccg ccaatgcttg cttctcggcg ggaagagggtg      300
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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/658,835  
 DATE: 09/22/2000  
 TIME: 14:59:33  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/658,835

DATE: 09/22/2000

TIME: 11:59:33

Input Set : A:\1134RSEQLIST.TXT

Output Set: N:\CRF3\09222000\I658835.raw

130	130	135	140	
132	ctc gac agt gta agc ttc ggc cac tac tgt gag aag gaa cta aac ttg			180
133	Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Leu Asn Leu			
134	145	150	155	160
136	ccg gct gtt ctc ggc gta gca aac cag atc aca cgc gct cta ctc ggt			628
137	Pro Ala Val Leu Cys Val Ala Asn Cln Ile Thr Arg Ala Leu Leu Gly			
138	165	170	175	
140	gtg gaa gcc cac gaa atc acc atg ctt ttg ctc acc gac tac atc aag			676
141	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys			
142	180	185	190	
144	agt gcc acc ggt ctc agt aat att ttc tgg cac aag aaa gac ggc ggc			621
145	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
146	195	200	205	
148	cag tat atg cga tgc aaa acg ggt atc gag tgg att tgc cat gcc atg			672
149	Gln Tyr Met Asn Cln Lys Thr Gly Met Gln Ser Ile Cys His Ala Met			
150	210	215	220	
152	tca aag gaa ctt gtt cca ggc tgc gta cac ctc aac acc ccc gtc gct			720
153	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala			
154	225	230	235	240
156	gaa att gag cac tgc gca tgc ggc tgt aca gta cga tgg gcc tgc ggc			768
157	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly			
158	245	250	255	
160	gcc gtg ttc cga acc aaa aac gta ctc gtt tgg tta ccg aca acc ttg			816
161	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu			
162	260	265	270	
164	tat ccc acc ttg aca ttt tca cca cct ttt ccc gcc gag aag caa gca			864
165	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala			
166	275	280	285	
168	ttg ggc gaa aat tct atc ctc ggc tac tat agc aag ata gtc ttc gta			912
169	Leu Ala Gln Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val			
170	290	295	300	
172	tgg gac aag ccg tgg tgg cgt gaa caa ggc ttc tgg ggc gtc ctc caa			960
173	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln			
174	305	310	315	320
176	tgg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc			1008
177	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val			
178	325	330	335	
180	gat cga caa tgg ttc att acc tgt ttc atg gtc gga gac ccg gga cgg			1056
181	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg			
182	340	345	350	
184	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac			1104
185	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp			
186	355	360	365	
188	caa ctc cgc gca gcc tac gag aac gcc ggc gcc caa gtc cca gag ccg			1152
189	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro			
190	370	375	380	
192	gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa gga			1200
193	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly			
194	385	390	395	400

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/658,835

DATE: 09/22/2000

TIME: 11:59:33

Input Set : A:\1134RSEQLIST.TXT

Output Set : N:\CRF3\09222000\I658835.raw

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196 ggt ccc agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcc 1218
197 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
198 405 410 415
200 ggg ctc aga acc ccc ttc aag aat gtt cat ttc att aga acc aag aag 1296
201 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
202 420 425 430
204 tct tta gtt tgg aac ggg tat atg gaa ggg acc ata cga tcc aat caa 1344
205 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
206 435 440 445
208 cga ggt gct gcc gaa gtt gtg gcc acc ctg gtg cca gcc aca 1386
209 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
210 450 455 460
211 tag 1389
212 210- SEQ ID NO: 6
213 211- LENGTH: 462
214 212- TYPE: PRT
215 213- ORGANISM: Exophiala spinitera
216 2100- SEQUENCE: 6
217 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
218 1 5 10 15
219 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
220 20 25 30
221 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
222 35 40 45
223 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
224 50 55 60
225 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
226 65 70 75 80
227 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
228 85 90 95
229 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
230 100 105 110
231 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
232 115 120 125
233 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
234 130 135 140
235 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
236 145 150 155 160
237 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
238 165 170 175
239 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
240 180 185 190
241 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
242 195 200 205
243 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
244 210 215 220
245 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
246 225 230 235 240
247 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly

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## RAW SEQUENCE LISTING

DATE: 09/22/2000

PATENT APPLICATION: US/09/658,835

TIME: 14:59:33

Input Set : A:\1134RSEQLIST.TXT

Output Set: N:\CRF3\09222000\I658835.raw

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251                               245                               250                               255
252 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
253                               260                               265                               270
254 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
255                               275                               280                               285
256 Leu Ala Glu Asn Ser Ile Leu Glu Tyr Tyr Ser Lys Ile Val Phe Val
257                               290                               295                               300
258 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
259                               305                               310                               315
260 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
261                               320                               325                               330
262 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
263                               335                               340                               345
264 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
265                               350                               355                               360
266 Gln Leu Arg Ala Ala Tyr Gln Asn Ala Gly Ala Gln Val Pro Glu Pro
267                               365                               370                               375
268 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
269                               380                               385                               390
270 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
271                               395                               400                               405
272 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Gln Thr
273                               410                               415                               420
274 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
275                               425                               430                               435
276 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
277                               440                               445                               450
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280 <12> TYPE: DNA
281 <13> ORGANISM: Exophiala spinifera
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285 <17> NAME/KEY: intron
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291 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
292 1 5 10 15
293 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
294 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
295 20 25 30
296 gag gcg atg cat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
297 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
298 35 40 45
299 ccc ggc agg acg act atc aac gac ctc jgc gct gcg tgg atc aat gac 192

```

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P. 6

&lt;210&gt; 19 Seq # 14

&lt;211&gt; 692

&lt;212&gt; PRT

&lt;213&gt; Unknown

M. was made to, &lt;210&gt; to &lt;213&gt;

-&gt; transfer to caption unknown

&lt;400&gt; 19

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
1				5				10						15	
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20					25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
			35				40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
			50			55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
					70					75				80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	

Organism: Sen

# 12 on line

Summary Sheet.

(Entire sequence not shown)



This error was  
also indicated in  
Sequence numbers:  
21, 25, 27, 29, 31, and  
33. Please review  
and correct.



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P 7

<210> 20 Seq # 20  
<211> 1464  
<212> DNA  
<213> Unknown

<220>

<223> Nucleotide sequence of K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464, trAPAO cDNA.



For the sequence rules, <223> feature is allowed a maximum number of 4 lines, 72 spaces per line. This error is also indicated in sequence # 30.

F.Y.I. ↓

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 09/22/2000

PATENT APPLICATION: US/09/658,835

TIME: 14:59:34

Input Set : A:\1134RSEQLIST.TXT

Output Set: N:\CRF3\09222000\I658835.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No  
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:49 M:341 W: (16) "n" or "Xaa" used, for SEQ ID#:1  
L:248 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7  
L:252 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7  
L:1237 M:253 W: Mandatory Feature missing, <220> FEATURE:  
L:1237 M:253 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1337 M:253 W: Field exceeds allowed number of lines, <223> Other Information:  
L:1338 M:253 W: Field exceeds allowed number of lines, <223> Other Information:  
L:1491 M:253 W: Mandatory Feature missing, <223> OTHER INFORMATION: 2;  
L:1508 M:253 W: Mandatory Feature missing, <223> OTHER INFORMATION: 2;  
L:1520 M:253 W: Mandatory Feature missing, <223> OTHER INFORMATION: 2;  
L:1592 M:253 W: Mandatory Feature missing, <220> FEATURE:  
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L:156 M:253 W: Field exceeds allowed number of lines, <223> Other Information:  
L:157 M:253 W: Field exceeds allowed number of lines, <223> Other Information:  
L:1490 M:253 W: Mandatory Feature missing, <220> FEATURE:  
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L:1818 M:253 W: Mandatory Feature missing, <220> FEATURE:  
L:1818 M:253 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1189 M:341 W: (16) "n" or "Xaa" used, for SEQ ID#:39  
L:1250 M:341 W: (16) "n" or "Xaa" used, for SEQ ID#:40